



SEQUENCE LISTING

<110> NIPPON MEDICAL SCHOOL

<120> Fusion cell death inducing gene specifically acting on
vascularizing endothelial cells

<130> P02-1021

<140>

<141>

<160> 27

<170> PatentIn Ver. 2.1

<210> 1

<211> 579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (579)

<400> 1

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Met Asp Gly Ser Gly Glu Gln Pro Arg Gly Gly Gly Pro Thr Ser Ser
1 5 10 15

gag cag atc atg aag aca ggg gcc ctt ttg ctt cag ggt ttc atc cag 96

Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln
20 25 30

gat cga gca ggg cga atg ggg ggg gag gca ccc gag ctg gcc ctg gac 144
Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp
35 40 45

ccg gtg cct cag gat gcg tcc acc aag aag ctg agc gag tgt ctc aag 192
Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys
50 55 60

cgc atc ggg gac gaa ctg gac agt aac atg gag ctg cag agg atg att 240
Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile
65 70 75 80

gcc gcc gtg gac aca gac tcc ccc cga gag gtc ttt ttc cga gtg gca 288
Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala
85 90 95

gct gac atg ttt tct gac ggc aac ttc aac tgg ggc cgg gtt gtc gcc 336
Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala
100 105 110

ctt ttc tac ttt gcc agc aaa ctg gtg ctc aag gcc ctg tgc acc aag 384
Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys
115 120 125

gtg ccg gaa ctg atc aga acc atc atg ggc tgg aca ttg gac ttc ctc 432
Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu
130 135 140

cgg gag cgg ctg ttg ggc tgg atc caa gac cag ggt ggt tgg gac ggc 480
 Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly
 145 150 155 160

ctc ctc tcc tac ttt ggg acg ccc acg tgg cag acc gtg acc atc ttt 528
 Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe
 165 170 175

gtg gcg gga gtg ctc acc gcc tcg ctc acc atc tgg aag aag atg ggc 576
 Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly
 180 185 190

tga 579

<210> 2

<211> 192

<212> PRT

<213> Homo sapiens

<400> 2

Met Asp Gly Ser Gly Glu Gln Pro Arg Gly Gly Gly Pro Thr Ser Ser
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 Glu Gln Ile Met Lys Thr Gly Ala Leu Leu Leu Gln Gly Phe Ile Gln
 20 25 30
 Asp Arg Ala Gly Arg Met Gly Gly Glu Ala Pro Glu Leu Ala Leu Asp
 35 40 45
 Pro Val Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys
 50 55 60

Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile
 65 70 75 80
 Ala Ala Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala
 85 90 95
 Ala Asp Met Phe Ser Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala
 100 105 110
 Leu Phe Tyr Phe Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys
 115 120 125
 Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu
 130 135 140
 Arg Glu Arg Leu Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly
 145 150 155 160
 Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe
 165 170 175
 Val Ala Gly Val Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly
 180 185 190

<210> 3

<211> 999

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(999)

<400> 3

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 1 5 10 15

ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg gaa ctg gat 96
 Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
 20 25 30

ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag ggt gaa ggt 144
 Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
 35 40 45

gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc acc act gga 192
 Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
 50 55 60

aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc acc tat ggc 240
 Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly
 65 70 75 80

gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag cat gac ttt 288
 Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe
 85 90 95

ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga acc atc ttt 336
 Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
 100 105 110

ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc aag ttc gaa 384
 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
 115 120 125

ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att gac ttt aag 432
 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
 130 135 140

gag gat gga aac att ctc ggc cac aag ctg gaa tac aac tat aac tcc 480
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
 145 150 155 160

cac aat gtg tac atc atg gcc gac aag caa aag aat ggc atc aag gtc 528
 His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
 165 170 175

aac ttc aag atc aga cac aac att gag gat gga tcc gtg cag ctg gcc 576
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
 180 185 190

gac cat tat caa cag aac act cca atc ggc gac ggc cct gtg ctc ctc 624
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 195 200 205

cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa gat ccc 672
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 210 215 220

aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc gct gct 720
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 225 230 235 240

ggg atc aca cat ggc atg gac gag ctg tac aag gcc ctt ttc tac ttt 768

Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe
245 250 255

gcc agc aaa ctg gtg ctc aag gcc ctg tgc acc aag gtg ccg gaa ctg 816
Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu
260 265 270

atc aga acc atc atg ggc tgg aca ttg gac ttc ctc cgg gag cgg ctg 864
Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu
275 280 285

ttg ggc tgg atc caa gac cag ggt ggt tgg gac ggc ctc ctc tcc tac 912
Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr
290 295 300

ttt ggg acg ccc acg tgg cag acc gtg acc atc ttt gtg gcg gga gtg 960
Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val
305 310 315 320

ctc acc gcc tca ctc acc atc tgg aag aag atg ggc tga 999
Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly
325 330

<210> 4

<211> 332

<212> PRT.

<213> Homo sapiens

<400> 4

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Phe	Thr	Gly	Val
Val	Pro	Ile	Leu
Val	Glu	Leu	Asp
20	25	30	
Gly	Asp	Val	Asn
Gly	His	Lys	Phe
Ser	Val	Ser	Gly
Glu	Gly	Glu	Gly
35	40	45	
Asp	Ala	Thr	Tyr
Gly	Lys	Leu	Thr
Leu	Lys	Phe	Ile
Cys	Thr	Thr	Gly
50	55	60	
Lys	Leu	Pro	Val
Pro	Trp	Pro	Thr
Leu	Val	Thr	Thr
Phe	Thr	Tyr	Gly
65	70	75	80
Val	Gln	Cys	Phe
Ser	Arg	Tyr	Pro
Asp	His	Met	Lys
Gln	His	Asp	Phe
85	90	95	
Phe	Lys	Ser	Ala
Met	Pro	Glu	Gly
Tyr	Val	Gln	Glu
Arg	Thr	Ile	Phe
100	105	110	
Phe	Lys	Asp	Asp
Gly	Asn	Tyr	Lys
Thr	Arg	Ala	Glu
Val	Lys	Phe	Glu
115	120	125	
Gly	Asp	Thr	Leu
Val	Asn	Arg	Ile
Glu	Leu	Lys	Gly
Ile	Asp	Phe	Lys
130	135	140	
Glu	Asp	Gly	Asn
Ile	Leu	Gly	His
Lys	Leu	Glu	Tyr
Asn	Tyr	Asn	Ser
145	150	155	160
His	Asn	Val	Tyr
Ile	Met	Ala	Asp
Lys	Gln	Lys	Asn
Gly	Ile	Lys	Val
165	170	175	
Asn	Phe	Lys	Ile
Arg	His	Asn	Ile
Glu	Asp	Gly	Ser
Val	Gln	Leu	Ala
180	185	190	
Asp	His	Tyr	Gln
Gln	Asn	Thr	Pro
Ile	Gly	Asp	Gly
Pro	Val	Leu	Leu
195	200	205	
Pro	Asp	Asn	His
Tyr	Leu	Ser	Thr
Gln	Ser	Ala	Leu
Ser	Lys	Asp	Pro
210	215	220	
Asn	Glu	Lys	Arg
Asp	His	Met	Val
Leu	Leu	Glu	Phe
Val	Thr	Ala	Ala
225	230	235	240
Gly	Ile	Thr	His
Gly	Met	Asp	Glu
Leu	Tyr	Lys	Ala
Leu	Phe	Tyr	Phe

	245	250	255
Ala Ser Lys Leu Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu			
260	265	270	
Ile Arg Thr Ile Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu			
275	280	285	
Leu Gly Trp Ile Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr			
290	295	300	
Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val			
305	310	315	320
Leu Thr Ala Ser Leu Thr Ile Trp Lys Lys Met Gly			
325	330		

<210> 5

<211> 987

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (987)

<400> 5

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ttc act ggc gtg gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat	96
Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn	

20	25	30	
ggg cac aaa ttt tct gtc agc gga gag ggt gaa ggt gat gcc aca tac	144		
Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr			
35	40	45	
gga aag ctc acc ctg aaa ttc atc tgc acc act gga aag ctc cct gtg	192		
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val			
50	55	60	
cca tgg cca aca ctg gtc act acc ttc acc tat ggc gtg cag tgc ttt	240		
Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Val Gln Cys Phe			
65	70	75	80
tcc aga tac cca gac cat atg aag cag cat gac ttt ttc aag agc gcc	288		
Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala			
85	90	95	
atg ccc gag ggc tat gtg cag gag aga acc atc ttt ttc aaa gat gac	336		
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp			
100	105	110	
ggg aac tac aag acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg	384		
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu			
115	120	125	
gtg aat aga atc gag ctg aag ggc att gac ttt aag gag gat gga aac	432		
Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn			
130	135	140	
att ctc ggc cac aag ctg gaa tac aac tat aac tcc cac aat gtg tac	480		

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
145 150 155 160

atc atg gcc gac aag caa aag aat ggc atc aag gtc aac ttc aag atc 528
Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
165 170 175

aga cac aac att gag gat gga tcc gtg cag ctg gcc gac cat tat caa 576
Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
180 185 190

cag aac act cca atc ggc gac ggc cct gtg ctc ctc cca gac aac cat 624
Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
195 200 205

tac ctg tcc acc cag tct gcc ctg tct aaa gat ccc aac gaa aag aga 672
Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
210 215 220

gac cac atg gtc ctg ctg gag ttt gtg acc gct gct ggg atc aca cat 720
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
225 230 235 240

ggc atg gac gag ctg tac aag gcc ctt ttc tac ttt gcc agc aaa ctg 768
Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe Ala Ser Lys Leu
245 250 255

gtg ctc aag gcc ctg tgc acc aag gtg ccg gaa ctg atc aga acc atc 816
Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile
260 265 270

atg ggc tgg aca ttg gac ttc ctc cgg gag cgg ctg ttg ggc tgg atc 864
 Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu Leu Gly Trp Ile
 275 280 285

caa gac cag ggt ggt tgg gac ggc ctc ctc tcc tac ttt ggg acg ccc 912
 Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr Phe Gly Thr Pro
 290 295 300

acg tgg cag acc gtg acc atc ttt gtg gcg gga gtg ctc acc gcc tca 960
 Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val Leu Thr Ala Ser
 305 310 315 320

ctc acc atc tgg aag aag atg ggc tga 987
 Leu Thr Ile Trp Lys Lys Met Gly
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<210> 6

<211> 328

<212> PRT

<213> Homo sapiens

<400> 6

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 Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
 35 40 45

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
 50 55 60
 Pro Trp Pro Thr Leu Val Thr Thr Phe Thr Tyr Gly Val Gln Cys Phe
 65 70 75 80
 Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
 85 90 95
 Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
 100 105 110
 Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
 115 120 125
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
 130 135 140
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
 145 150 155 160
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
 165 170 175
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
 180 185 190
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
 195 200 205
 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
 210 215 220
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His
 225 230 235 240
 Gly Met Asp Glu Leu Tyr Lys Ala Leu Phe Tyr Phe Ala Ser Lys Leu
 245 250 255
 Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile
 260 265 270
 Met Gly Trp Thr Leu Asp Phe Leu Arg Glu Arg Leu Leu Gly Trp Ile
 275 280 285

Gln Asp Gln Gly Gly Trp Asp Gly Leu Leu Ser Tyr Phe Gly Thr Pro
 290 295 300
 Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val Leu Thr Ala Ser
 305 310 315 320
 Leu Thr Ile Trp Lys Lys Met Gly
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<210> 7

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Homing peptide

<400> 7

Cys Leu Ser Ser Arg Leu Asp Ala Cys

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<210> 8

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 8

Cys Asn Ser Arg Leu His Leu Arg Cys

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<210> 9

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 9

Cys Glu Asn Trp Trp Gly Asp Val Cys

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<210> 10

<211> 21

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 10

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10

15

Asn Arg His Arg Leu

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<210> 11

<211> 7

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 11

Cys Leu Pro Val Ala Ser Cys

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<210> 12

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 12

Cys Gly Ala Arg Glu Met Cys

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<210> 13

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 13

Cys Lys Ser Thr His Asp Arg Leu Cys

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<210> 14

<211> 9

<212> PRT

<213> Artificial Sequence

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<210> 15

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

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Ala Pro Arg Pro Gly

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<210> 16

<211> 6

<212> PRT

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<223> Description of Artificial Sequence:Homing peptide

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Lys Gln Ala Gly Asp Val

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<210> 17

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 17

Lys Arg Leu Asp Gly Ser

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<210> 18

<211> 4

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Homing peptide

<400> 18

Asp Gly Glu Ala

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<210> 19

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

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<221> misc_feature

<222> (1).. (2)

<223> n is A, C, G or T

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28

<210> 20

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 20

ctggcaaagt agaaaagggc cttgtacagc tcgtc 35

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 21

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<210> 22

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

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<222> (1).. (2)

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<400> 22

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26

<210> 23

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 23

ccatggcctg cgattgccgt ggtgattgtt tttgtggtgg tatgagcaag ggcgagg

57

<210> 24

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

<220>

<221> misc_feature

<222> (1).. (4)

<223> n is A, C, G or T

<400> 24

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<210> 25

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 25

tggaaaagca ctgcacgc

18

<210> 26

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 26

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<210> 27

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

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<221> misc_feature

<222> (1)..(4)

<223> n is A, C, G or T

<400> 27

nnnnccatgg cctgcaacgg tc

22